

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 5, 2003, 02:50:22 ; Search time 1526 Seconds  
(without alignments)  
4669.734 Million cell updates/sec

Title: US-09-847-081B-2  
Perfect score: 2270  
Sequence: 1 MSMSVALLWVSTSEVSNGL.....IAYAKSLVPPNRTSSPLAKT 440

Scoring table:  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlip  
-O=/cgn2.1/USPTO.spool/US09847081/runat\_01042003.120129.26749/app\_query.fasta\_1.583  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09847081 -CGN\_1.1.2874.0runat\_01042003.120129.26749 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1211	53.0	1655	11	AY111032 Zea mays
2	1202	53.3	787	13	BM410846 EST585173
3	1201.5	52.9	1201	11	AY108547 Zea mays
c	1179	51.9	781	14	BQ511016 EST618431
5	1136	50.0	751	14	BQ046203 EST595321
6	1130	49.8	765	13	BM408984 EST583311
7	1099	48.4	686	10	AW442101 EST311497
8	1083	47.7	682	13	BM409200 EST583527
9	1072	47.2	672	10	AW442407 EST311803
10	1049	46.2	642	10	BE433198 EST399727
11	1043	45.9	676	10	AW222027 EST298838
12	1001	44.1	677	12	BG351357 104A12 Ma
13	997	43.9	634	13	BM412533 EST586660
14	980	43.2	600	10	BE460889 EST412308
15	977.5	43.1	623	10	BE432511 EST399040
16	956	42.1	685	10	AW221932 EST298743
17	947	41.7	582	10	AW223316 EST300127
18	940	41.4	581	10	BE432955 EST399484
19	939	41.4	623	13	BM536249 EST589271
20	934	41.1	582	10	AW223666 EST300477
21	927	40.8	605	10	BE435064 EST406142
22	927	40.8	744	13	BM412719 EST587057
23	921	40.6	562	10	BE433966 EST405044
24	918	40.4	634	13	BM137086 WHE2629.C
25	917	40.4	565	10	BE432595 EST399124
26	916	40.4	573	10	BE435308 EST406386
27	913	40.2	585	10	AW222245 EST399056
28	907	40.0	668	13	B1955682 HVSME002
29	899	39.6	556	10	AW222152 EST298963
30	897	39.3	609	10	BE322877 NF048H11
31	891	39.3	581	10	AW222806 EST299617
32	884	38.9	645	10	AW496851 9a49b02.Y
33	884	38.9	791	10	AW223528 EST300339
34	881	38.8	542	10	BE431550 EST333635
35	879	38.7	613	13	B1957464 HVSME000
36	877	38.6	543	13	BM411875 EST586202
37	873	38.5	634	10	AW441216 EST310812
38	873	38.5	687	10	BE434578 EST405656
39	870	38.3	542	10	BE432748 EST399277
40	867	38.2	563	10	BE461396 EST411815
41	865	38.1	555	10	BE460463 EST411882
42	860	37.9	566	12	BF112979 EST440862
43	858	37.8	536	10	BE434911 EST405989
44	856	37.7	563	10	BE437095 EST408213
45	848	37.4	551	10	BE432084 EST398613

# ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	ALIGNMENTS
AY111032	Zea mays	1655 bp	CL1906_1	mRNA sequence.				
AY111032	Zea mays		AY111032					
AY111032.1	HTC		GI:21215622					
Zea mays								
Zea mays								
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC								
Clade; Panicoideae; Andropogoneae; Zea.								
1 (bases 1 to 1655)								
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.								





```

Db 527 GTCTGGGCTCGCTCCGACTCCAGGCTCGACCGAGCGTGATCATGCTGCTCTG 586
QY 300 AlaleuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgaspValGlyGluAspAlaArg 319
Db 587 GCTCTGGCATCGCTTAACCAAGCTGACCAATATCTCAGAGACGTGGCGAAGATGCGAGG 646
QY 320 ArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAsp 339
Db 647 AGGGGAGATATACCTTCGCTGGACGACGCTGGCGAGCGAGCTCAGCGAAGAGGAC 706
QY 340 IlePheAlaGlyArgValThrAspLysTyrArgAsnPheMetLysLysGlnIleGlnArg 359
Db 707 ATATTCAAGGGAAGTGACCGCAAGTGGAGGAGGTTCATGAAGGCGCAGATCCACGCT 766
QY 360 AlaArgLysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArg 379
Db 767 GCCAGGCTCTCTTTGATGAGGCGGAGAGGCGTCAACCATCTCGACTCTGCTAGCAGA 826
QY 380 TrpProValLeuThrAlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsn 399
Db 827 TGGCGGTGCTCGGCTCTGTGGCTGTACAGCGAGATCCTTGTATGCCATGTAGGCAAC 886
QY 400 AspTyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeu 419
Db 887 GACTACAACAACCTTCAACCAAGCGTGGTACGCGCAAGCGCCAGAGAGCTGCTGCTGA 946
QY 420 ProIleAlaTyrAlaLysSerLeuValProPro 430
Db 947 CCGCTTCATATGCAAGGCGTGGGTGCACCA 979

```

```

RESULT 4
BO511016/c 781 bp mRNA linear EST 22-JUL-2002
LOCUS EST618431 Generation of a set of potato cDNA clones for microarray
DEFINITION analyses mixed potato tissues Solanum tuberosum cDNA clone STMH067
3' end, mRNA sequence.
ACCESSION BO511016
VERSION BO511016.2 GI:21926690
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 781)
AUTHORS Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
Karamecheva,S.A.
TITLE Generation of a set of potato cDNA clones for microarray analyses
JOURNAL Unpublished (2002)
COMMENT On Jun 10, 2002 this sequence version replaced gi:21369885.
Other_ESTs: EST618430
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato@igr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cdna@resgen.com
Seq primer: T7.

```

```

FEATURES
SOURCE
Location/Qualifiers
1..781
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjite"
/db_xref="taxon:4113"
/clone="STMH067"
/clone_lib="Generation of a set of potato cDNA clones for
microarray analyses mixed potato tissues"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora

```

```

infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes,
tubers, or roots."
BASE COUNT 202 a 191 c 144 g 244 t
ORIGIN
Alignment Scores:
Pred. No.: 4,78e-135 Length: 781
Score: 1179.00 Matches: 230
Percent Similarity: 96.36% Conservativeness: 8
Best Local Similarity: 93.12% Mismatches: 9
Query Match: 51.94% Indels: 1
DB: 14 Gaps: 0

```

US-09-847-081b-2 (1-440) x BO511016 (1-781)

```

QY 194 AsnAlaSerHisIleThrProGlnAlaLeuAspArgTyrGluThrArgLeuGluAspIle 213
Db 781 AATGCATCACACATACTCCACAGCTTTAGATAGTGGGAGGCCAGCTGGAAGATAT - 723
QY 214 PheSerGlyArgPropheAspMetLeuAspAlaLeuSerAspThrValSerArgPhe 233
Db 722 TTCAACGGCGCGCATTTGATATGCTGATGCAGCTTTATCCGATCTGTTTCCAAATT 663
QY 234 ProValAspIleGlnPropheArgAspMetIleGluGlyMetArgMetAspLeuTrpLys 253
Db 662 CCGTGTGATATTCAGCCATTTCAGAGATATGTTGAAAGGAATGCGTATGCGTGTGGA 603
QY 254 SerArgTyrLysThrPheAspGluLeuTyrLeuTyrCysTyrValAlaGlyThrVal 273
Db 602 TCAGATACACAACACTTTGATGAATATCTATATGTTACTATGTCGCTGGTACAGTA 543
QY 274 GlyLeuMetSerValProValMetGlyIleAlaProGluSerLysAlaThrGluSer 293
Db 542 GGATGTGATGAGTGTCCAAATTATGGCATTGCACCTGAATCAAGGAACACAGAGAGT 483
QY 294 ValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgasp 313
Db 482 GTATATAACGACGCTTTGGCTTTAGGGATCGCAAACTCAACTAATATATCTACAGAGAT 423
QY 314 ValGlyGluAspAlaArgArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAla 333
Db 422 GTAGGAGAAGATGCAAGAGAGGAGAGATATCTACTCAAGATGAATATAGCACAGCA 363
QY 334 GlyLeuSerAspGluAspIlePheAlaGlyArgValThrAspLysTyrArgAsnPheMet 353
Db 362 GGGCTCTCCGATGAAGACATTTTGGCTGGAAGAGTACTGATAAGTGGAGGATCTTTATG 303
QY 354 LysLysGlnIleGlnArgAlaArgLysPheAspGluSerGluLysGlyValThrGlu 373
Db 302 AAGAAGCAAATTCAGAGGGCAAGAAATCTTTGATGAGGAGCAAAAGGTTGTACACAGA 243
QY 374 LeuAspSerAlaSerArgTyrProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeu 393
Db 242 CTGAGCTCTGCTAGTAGTGGCGGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
QY 394 AspGluIleGluAlaAsnAspTyrAsnAsnPheThrArgArgAlaTyrValSerLysPro 413
Db 182 GACGAGATTCAAGGAAGAGGACTACAACAACCTTCAAGAGGGGCTTATGTGAGCAAGCA 123
QY 414 LysLysLeuLeuThrLeuProIleAlaTyrAlaLysSerLeuValProProAsnArgThr 433
Db 122 AAGAAGCTTCTGACGTTGCCCATTTGCTTATGCAAGATCTCTAGTGGCCCCCTTAAGTCAACT 63
QY 434 SerSerProLeuAlaLysThr 440
Db 62 TCCTCCCACTAGCAAGAGACA 42

```

RESULT 5

BO046203

LOCUS

DEFINITION

Reaction Solanum tuberosum cDNA clone BPL114E21 5' end, mRNA

BO046203 751 bp mRNA linear EST 29-MAR-2002  
EST595321 P. infestans-challenged potato leaf, incompatible  
reaction Solanum tuberosum cDNA clone BPL114E21 5' end, mRNA

```

sequence.
BQ046203
VERSION BQ046203.1 GI:19820189
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum

REFERENCE
AUTHORS Zhang,P., Hernandez,M., Tornqvist,C.-E., Wirtz,U., Loukianov,A.,
Rangel,P., Haberlach,G.T., Karanicheva,S.A., Tsai,J., Chieningo,A.,
Bougri,O., Buell,C.R., Ronning,C.M., Helgeson,J. and Baker,B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, incompatible interaction (2002)
JOURNAL Unpublished (2002)
COMMENT Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: T3.
FEATURES
source Location/Qualifiers
1..751
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="BPL114E21"
/clone_lib="P. infestans-challenged potato leaf,
incompatible reaction"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: UC Berkeley, PGEC; sequencing: The
Institute for Genomic Research. Whole plants were
challenged with 450,000 sporangia/ml P. infestans isolate
US-1 (US940501) in Biotron (Madison, Wisconsin). Leaf
tissue was collected at 1, 2, 5, 12, and 24 hours
post-challenge and frozen in liquid nitrogen immediately
upon removal. Kennebec plants showed no signs of HR.
Katahdin plants (susceptible to P. infestans US-1) were
used as controls and showed infection. NOTE: We cannot
exclude the possibility that this sequence is actually
derived from Phytophthora rather than potato."
BASE COUNT 219 a 119 c 214 t
ORIGIN
Alignment Scores:
Pred. No.: 9.55e-130 Length: 751
Score: 1136.00 Matches: 225
Percent Similarity: 94.40% Conservative: 11
Best Local Similarity: 90.00% Mismatches: 12
Query Match: 50.04% Indels: 3
DB: 14 Gaps: 0

US-09-847-081b-2 (1-440) x BQ046203 (1-751)

Qy 67 AlaaspProArgTyrSerCysLeuGlyGlySerArgThrGluLysGlySerThrPheSer 86
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 5 GCAGATTTCAGATATTCGTGTTTAGGAGATCAAGAACTGAGATGGAAGGATTTTCT 64

Qy 87 ValGlnSerLeuValAlaSerProAlaGlyGluMetThrValSerSerGluLysLys 106
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 65 GTACAGTCCAGTTGGTGGCTAGTCCAGCTGGAGAAATGGCTGTCTATCAGAAAG 124

Qy 107 ValTyraspValValLeuLysGlnAlaLeuValLysArgGlnLeuArgSerThrAsp 126
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 125 GTGTATGAGGTGGTATTGAGCAGGCGACTTTAGTGAAGAGGCATCTCATATCTACTG 184

Qy 127 AspLeuGluValLysProAspIleValValProGlyAsnLeuGlyLeuLeuSerGluAla 146
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 185 GACATAGAAGTGAAGCGGATATTGTTGCCGGTAATTTGGGCTTTGTTGATGAAGCA 244

```

```

Qy 147 TyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyrLeuGlyThrLys 166
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 245 TATGATCGTTGTCGGGAGTAGTGTGCAGATATGCTAGACATTTTACTTAGGACCATG 304

Qy 167 LeuMetThrProGluArgArgAlaIleTrpAlaIleTyrValTyrCysArgThr 186
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 305 CTAATGACTCCAGACAGAGAAGAGACTATCTGGGCAATATATGTGTGGTGCAGGAACT 364

Qy 187 AspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTyr 206
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 365 GATGAGCTTGTGTATGGCCCTTAATGCATCACACATAATCCACAAGCTTTAGTAGGTGG 424

Qy 207 GluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAlaLeu 226
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 425 GAGCCAGGCTGGAGATATTTTCAACGGCGGCCATTTGATATGCTTGATCGACCTTGA 484

Qy 227 SerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGly 246
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 485 TCCGATACGTGTTCCAAATTCCTGTTGATATTCAGCCATTTCAGAGATATGTTGAAGA 544

Qy 247 MetArgMetAspLeuTyrLysSerArgTyrLysThrPheAspGluLeuTyrLeuTyrCys 266
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 545 ATGCGTATGGACTTGTGGAAATCCAGATACACAACATTTGATGAACATATATCTATTGT 604

Qy 267 TyrTyrValAlaGlyThrValGly-LeuMetSerValProValMetGlyIleAlaProGln 286
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 605 TACTATGTCGTCGTACAGTAGGATTTGATGAGTGTTCATATTTGGCATTTGGACCTGA 664

Qy 286 userLysAlaThrThrGluSerValTyrAsnAlaAla-LeuAlaLeuGlyLeuAlaAsnG 306
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 665 ATCCAAGCAACAGACAGAGTGTATATAAGCAGCTTTTGGCTTTAGGGATCGCCAATC 724

Qy 306 InLeuThrAsnIleLeuArgAspVal 314
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 725 AACTAACCAT-ATACTCAAGATGTA 749

RESULT 6
LOCUS BM408984 765 bp mRNA linear EST 22-JAN-2002
DEFINITION EST593311 tomato breaker fruit Lycopersicon esculentum cDNA clone
cLEG46P23 5' end, mRNA sequence.
ACCESSION BM408984
VERSION BM408984.1 GI:18260614
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 765)
AUTHORS Alcala,J., Vrebalov,J., White,R., Vision,T., Karanicheva,S.A., Tsai
,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
FEATURES
source Location/Qualifiers
1..765
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG46P23"
/tissue_type="tomato breaker fruit"

```

```

/dev_stage="breaker"
/lab_host="SOLR"
/notes=Vector: pBluescriptSKmCuadap; Site_1: EcoRI;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp.

```

```

BASE COUNT 237 a 122 c 202 g 204 t
ORIGIN

```

```

Alignment Scores:
Pred. No.: 5,45e-129 Length: 765
Score: 1130.00 Matches: 222
Percent Similarity: 90.94% Conservative: 9
Best Local Similarity: 87.40% Mismatches: 20
Query Match: 49.78% Indels: 3
DB: 13 Gaps: 2

```

```

US-09-847-081B-2 (1-440) x BM408984 (1-765)

```

```

QY 128 LeuGluValLysProAspIleValValProGlyAsnLeuGlyLeuLeuSerGluAlaTyr 147
DB 1 TTAGAAGTGAAGCGGATATACCTATTCGCGGGAATTTGGCTGTGTGAGTGAGCATAT 60
QY 148 AspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeu 167
DB 61 GATAGGTGTGGTGAAGTATGTGCAGAGTATGCAAGACGTTTAACATTAGGAACATGCTA 120
QY 168 MetThrProGluArgArgAlaIleTyrAlaIleTyrValTyrCysArgGlyThrAsp 187
DB 121 ATGACTCCCGAGAGAGAGAGCGTATCTGGGCAATATATGTATGGTGCAGAAACAGAT 180
QY 188 GluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTyrGlu 207
DB 181 GAACCTTGTATGCGCCAAACGATCATATATACCCGCGCAGCTTAGATAGTGGAA 240
QY 208 ThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAlaLeuSer 227
DB 241 AATAGGCTAGAGATGTTTCAATGGCGGCCATTTGACATGTCGATGCTGTGTTGTC 300
QY 228 AspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGlyMet 247
DB 301 GATACAGTTTCTAACCTTCAGTATTCAGCCATTCAGACATATGATGAGGATG 360
QY 248 ArgMetAspLeuThrLysSerArgTyrLysThrPheAspGluLeuTyrLeuTyrCysTyr 267
DB 361 CGTATGGACTTGAGAAATCGAGATACAAAACTTCGACGAACATATACCTTTATGTTAT 420
QY 268 TyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGluSer 287
DB 421 TATGTTGCTGTCAGGTGGTGTGATGAGTGTCCCAATATATGGTATCGCCCTGAATCA 480
QY 288 LysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeu 307
DB 481 AAGCAACAACACAGAGCGTATATATGCTGCTTGGCTCTGGGATCGCAATCAATTA 540
QY 308 ThrAsnIleLeuArgAspValGlyGluAspAlaArgGlyArgValTyrLeuProGln 327
DB 541 ACTAACATCTCAGATGTTGGGAAGATGCCAGAAGAGAGAGAGTCTACTTGCCTCAA 600
QY 328 AspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGlyArgValThrAs 347
DB 601 GATGAATTACACAGCGAGCTCTATCCGATGAAGATATATTTGCTGGAGAGGTGACCGA 660
QY 347 pLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaAlaGlySerPheAspGluSe 367
DB 661 TAAATGAGAAATCTTATGAGAAACAA---TACTAGGCAAGAAAGTCTTTCATGAGCA 717
QY 367 rGluLysGlyValThrGluLeuAspSerAlaSerArgTyr 380
DB 718 GAGAAAGCGT---GACAGATGAGCTCAGCTAGTAGATTC 754

```

```

RESULT 7
AW442101 686 bp mRNA linear EST 18-MAY-2001
LOCUS EST311497 tomato fruit red ripe, TAMU Lycopersicon esculentum CDNA
DEFINITION clone cLEN21G20 5', mRNA sequence.
ACCESSION AW442101
VERSION AW442101.1 GI:6977352
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 686)
AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
Location/Qualifiers
1..686
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEN21G20"
/clone_lib="tomato fruit red ripe, TAMU"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
XhoI; supplier: pBluescript SK(-); Site_1: EcoRI; Site_2:
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 204 a 114 c 182 g 186 t
ORIGIN

```

```

Alignment Scores:
Pred. No.: 3.17e-125 Length: 686
Score: 1099.00 Matches: 209
Percent Similarity: 95.61% Conservative: 9
Best Local Similarity: 91.67% Mismatches: 10
Query Match: 48.41% Indels: 0
DB: 10 Gaps: 0

```

```

US-09-847-081B-2 (1-440) x AW442101 (1-686)

```

```

QY 108 TyrAspValValLeuLysGlnAlaAlaLeuValLysArgGlnLeuArgSerThrAsp 127
DB 2 TATGATGTGGTGTGGAGGAGGAGCGCTTGGTGAAGAGGCAACTGAGATCTACCAATGAG 61
QY 128 LeuGluValLysProAspIleValValProGlyAsnLeuGlyLeuLeuSerGluAlaTyr 147
DB 62 TTAGAAGTGAAGCGGATATACCTATTCGCGGGAATTTGGCTGTGTGAGTGAGCATAT 121
QY 148 AspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeu 167
DB 122 GATAGGTGTGGTGAAGTATGTGCAGAGTATGCAAGACGTTTAACATTAGGAACATGCTA 181
QY 168 MetThrProGluArgArgAlaIleTyrAlaIleTyrValTyrCysArgGlyThrAsp 187
DB 182 ATGACTCCCGAGAGAGAGAGCGTATCTGGGCAATATATGTATGGTGCAGAAACAGAT 241

```

QY 188 GluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTrpGlu 207  
 Db 242 GAACTTTGTTGATGGCCCAACGCATCATATATACCCGGCAGCTTAGATAGTGGAA 301  
 QY 208 ThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAlaLeuSer 227  
 Db 302 ATAGGCTAGAGATGTTTCAATGGCGGCCATTGACATGCTCGATGGTCTTGTC 361  
 QY 228 AspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGlyMet 247  
 Db 362 GATACAGTTTCAACTTCCAGTTGATATACGCCATTGAGATATGATTGAAGGATG 421  
 QY 248 ArgMetAspLeuTrpLysSerArgTrpLysThrPheAspGluLeuTrpLysCysTrp 267  
 Db 422 CGTATGGACTTGAGAAATTCGAGATACAAAACCTTCGACGAACATATACCTTTATTGTTAT 481  
 QY 268 TyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGluSer 287  
 Db 482 TATGTTGCTGGTACGGTTGGTGTGATGAGTGTTCCTATGATGGTATCCGCCCTGAATCA 541  
 QY 288 LysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeu 307  
 Db 542 AAGGCAACAACAGAGAGCGTATATATGCTGCTTGGCTCTGGGATCCCAATCAATTA 601  
 QY 308 ThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArgValTyrLeuProGln 327  
 Db 602 ACTAATACTCAGAGATGTTGGAGAAGATGCCAGAAGAGGAGTCTACTTGCCTCAA 661  
 QY 328 AspGluLeuAlaGlnAlaGlyLeu 335  
 Db 662 GATGAATTAACCGAGCGGTCTTA 685

## RESULT 8

BM409200 682 bp mRNA linear EST 22-JAN-2002  
 LOCUS EST583527 tomato breaker fruit Lycopersicon esculentum cDNA clone  
 DEFINITION CLE847J1 5' end, mRNA sequence.

ACCESSION BM409200  
 VERSION BM409200.1 GI:18260830  
 KEYWORDS EST.  
 SOURCE tomato.

## ORGANISM

Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

## REFERENCE

1 (bases 1 to 682)  
 Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai  
 ,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Renning  
 ,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.  
 Generation of ESTs from tomato fruit tissue, breaker stage (2002)  
 Unpublished (2002)

## COMMENT

Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 This clone is available through the Clemson University Genomics  
 Institute

## FEATURES

Seq primer: T3.  
 Location/Qualifiers

1..682  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA96"  
 /db\_xref="taxon:4081"  
 /clone="CLE847J1"  
 /tissue="tomato breaker fruit"  
 /dev\_stage="breaker"  
 /lab\_host="SOLN"  
 /note="Vector: pBluescriptSKmCUadapt; Site\_1: EcoRI;  
 Site\_2: XhoI; supplier: Boyce Thompson Institute;

sequencing: The Institute for Genomic Research. Fruit  
 were harvested at the breaker stage (first sign of  
 lycopene accumulation on the blossom end of fruit). Fruit  
 were cut in half and the seeds and locules were discarded  
 prior to freezing the pericarp.

BASE COUNT 217 a 114 c 173 g 178 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 3 02e-123 Length: 682  
 Score: 1083.00 Matches: 207  
 Percent Similarity: 94.71% Conservative: 8  
 Best Local Similarity: 91.19% Mismatches: 12  
 Query Match: 47.71% Indels: 0  
 DB: 13 Gaps: 0

US-09-847-081B-2 (1-440) x BM409200 (1-682)

QY 155 AlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArg 174  
 Db 1 GCAGAGTATGCAGAACGTTTAACTTAGGAACCTATGCTATGACTCCCGAGAGAAGG 60  
 QY 175 AlaIleTrpAlaIleTyrValTrpCysArgArgThrAspGluLeuValAspGlyProAsn 194  
 Db 61 GCTATCTGGCAATATATGATGTTGTCAGAGAACAAGATGAACCTTGTGTGATGCCCAAC 120  
 QY 195 AlaSerHisIleThrProGlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePhe 214  
 Db 121 GCATCATATATTACCCGGCAGCCTTAGTAGTGGGAAATAGGCTAGAGATGTTTC 180  
 QY 215 SerGlyArgProPheAspMetLeuAspAlaAlaLeuSerAspThrValSerArgPhePro 234  
 Db 181 AATGGCGGCCATTTGACATGCTCGATGGTGTGTTGTCGATACAGTTTCTAACTTTCCA 240  
 QY 235 ValAspIleGlnProPheArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSer 254  
 Db 241 GTTGATATTACCCATTCAGAGATATGATTGAAGGAATGCGTATGGACTTCAGAAAATCG 300  
 QY 255 ArgTyrLysThrPheAspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGly 274  
 Db 301 ACATACAAAACCTCCGACCAACTATACCTTTATTTATTTGCTGTCGATGGG 360  
 QY 275 LeuMetSerValProValMetGlyIleAlaProGluSerLysAlaThrThrGluSerVal 294  
 Db 361 TTGATGAGTGTTCATTTATGGTATCGCCCTGATCAAGGCAACACAGAGAGCGTA 420  
 QY 295 TyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspVal 314  
 Db 421 TATAATGCTGCTTGGCTCTGGGGATCGCAAAATCAATTAACATACATCTCAGAGATGT 480  
 QY 315 GlyGluAspAlaArgArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGly 334  
 Db 481 GGAGAAGATGCCAAGAGAGAGAGTCTCTCTCCCAAGATGAATATATCACAGGAGGT 540  
 QY 335 LeuSerAspGluAspIlePheAlaGlyArgValThrAspLysTrpArgAsnPheMetLys 354  
 Db 541 CTATCCGATGAGATATATTGCTGGAGGGTGACCGATAAATGGAGAACTTTATTCAG 600  
 QY 355 LysGlnIleGlnArgAlaArgLysPheAspGluSerGluLysGlyValThrGluLeu 374  
 Db 601 AAACAAATACATAGGCAAGAAAGTCTTTTGTATGAGGAGAGAGAAGCGCTGACAGAAATTG 660  
 QY 375 AspSerAlaSerArgTrpPro 381  
 Db 661 AGCTCAGCTAGTAGATTCCT 681

## RESULT 9

AW442407  
 LOCUS AW442407  
 DEFINITION EST311803 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA  
 clone cLEN22L14 5', mRNA sequence.  
 ACCESSION AW442407  
 VERSION AW442407.1 GI:6977658

672 bp mRNA linear EST 18-MAY-2001



```

KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum.
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
          Lycopersicon.
1 (bases 1 to 672)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F.,
Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M.,
Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: CUGI
Location/Qualifiers
  1. 672
  /organism="Lycopersicon esculentum"
  /cultivar="TA496"
  /db_xref="taxon:4081"
  /clone="cLEN22L14"
  /clone_lib="tomato fruit red ripe, TAMU"
  /tissue_type="pericarp"
  /dev_stage="red ripe (7-20 days post-breaker)"
  /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
  xhoI; supplier: Giovannoni; Fruit were tagged at the
  breaker stage (first sign of lycopene accumulation on the
  blossom end of the fruit) and harvested 7 days
  post-breaker (fully red-ripe), 10 days post breaker, and
  20 days post-breaker (over-ripe). 20 day fruit which
  showed external or internal signs of pathogenesis were
  discarded. Fruit were cut in half and the seeds and
  locules were discarded prior to freezing the pericarp."
  212 a 112 c 170 g 178 t

BASE COUNT 212 a 112 c 170 g 178 t
ORIGIN

Alignment Scores:
Pred. No.: 6.79e-122 Length: 672
Score: 1072.00 Matches: 205
Percent Similarity: 95.07% Conservative: 7
Best Local Similarity: 91.93% Mismatches: 11
Query Match: 47.22% Indels: 0
DB: 10 Gaps: 0

US-09-847-081B-2 (1-440) x AW442407 (1-672)

QY 160 ThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIle 179
Db 3 ACGTTTAACCTAGGAACATGCTATGATCCCGAGAGAAGAGGCTATCTGGCAATA 62
QY 180 TyrValTyrCysArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThr 199
Db 63 TATGTATGGTCGAGAGACAGATGACATGTTGTATGCCCAACGATCATATATTACC 122
QY 200 ProGlnAlaLeuAspArgTTPGluThrArgLeuGluAspIlePheSerGlyArgProPhe 219
Db 123 CGGCAGCGCTAGATAGTGGGAAATAGGCTAGAGATGTTTCAATGGCGGCATT 182
QY 220 AspMetLeuAspAlaAlaLeuSerAspThrValSerArgProValAspIleGlnPro 239
Db 183 GACATGCTCGATGGTCTTTCGATACAGTTTCTCACTTTCCAGTTGATATTCAGCCA 242
QY 240 PheArgAspMetIleGluGlyMetArgMetAspLeuTyrLysSerArgTyrLysThrPhe 259
Db 243 TTCAGAGATATGATGAGAGATGCGTATGGCTTGGAGAAATCGAGATACAAACATTC 302
QY 260 AspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValPro 279
Db 303 GACGAACATATACCTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 362

```

```

QY 280 ValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaLeu 299
Db 363 ATTATGGGTATGCCCTGAATCAAGGCAACAAGAGAGGCTATATATGCTGCTTTC 422
QY 300 AlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArg 319
Db 423 GCTCTGGGATCGCAATCAATTAACATACTACAGATGTTTGGAGAAGATGCCAGA 482
QY 320 ArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAsp 339
Db 483 AGAGGAAGAGTCTACTTGCCTCAAGATGAATAGCACAGGCGTATCCGATGAAGAT 542
QY 340 IlePheAlaGlyArgValThrAspLysTyrArgAspPheMetLysLysGlnIleGlnArg 359
Db 543 ATATTGCTGGAGGGTGNCCGATAATGGAGAATCTTTATGAGAAACAATACATAGG 602
QY 360 AlaArgLysPheAspGluSerGlyLysGlyValThrGluLeuAspSerAlaSerArg 379
Db 603 GCAGAAAGTTCTTTGATGAGGAGAGAAAGCGTGACAGAAATGAGCTCAGCTAGATA 662
QY 380 TrpProVal 382
Db 663 TTCCTGTGA 671

RESULT 10
LOCUS BE433198 642 bp mRNA linear EST 18-MAY-2001
DEFINITION ESN399727 tomato breaker fruit, TIGR Lycopersicon esculentum CDNA
ACCESSION BE433198
VERSION BE433198.1 GI:9431041
KEYWORDS EST
SOURCE tomato.
ORGANISM Lycopersicon esculentum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
          Lycopersicon.
1 (bases 1 to 642)
Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
, S.D.
Generation of ESTs from tomato fruit tissue, breaker stage
Unpublished (2000)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
  1. 642
  /organism="Lycopersicon esculentum"
  /cultivar="TA496"
  /db_xref="taxon:4081"
  /clone="cLEG12N5"
  /clone_lib="tomato breaker fruit, TIGR"
  /tissue_type="pericarp"
  /dev_stage="breaker"
  /lab_host="SOLR"
  /note="Vector: pBluescriptSKMuadapt; Site_1: EcoRI;
  Site_2: XhoI; Fruit were harvested at the breaker stage
  (first sign of lycopene accumulation on the blossom end of
  the fruit). Fruit were cut in half and the seeds and
  locules were discarded prior to freezing the pericarp."
  194 a 103 c 167 g 178 t

BASE COUNT 194 a 103 c 167 g 178 t
ORIGIN

Alignment Scores:
Pred. No.: 4.47e-119 Length: 642
Score: 1049.00 Matches: 199

```



Percent Similarity: 95.77% Conservative: 5  
 Best Local Similarity: 93.43% Mismatches: 9  
 Query Match: 46.21% Indels: 0  
 DB: 10 Gaps: 0

US-09-847-081B-2 (1-440) x BE433198 (1-642)

QY 140 LeuGlyLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLys 159  
 Db 2 TTGGGCTGTGAGTGAACATATGATAGTGTGGTGAAGATATGTCAGAGTATGCAAG 61  
 QY 160 ThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleThrPalalile 179  
 Db 62 ACCTTTAACTAGCACTATGCTATGACTCCCGAGAGAGAGGGCTATCTGGCAATA 121  
 QY 180 TyrValTrpCysArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThr 199  
 Db 122 TATGTATGGTGCAGAGACAGATGAACCTGTTGATGGCCCAACGCATCATATATACC 181  
 QY 200 ProGluAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProphe 219  
 Db 182 CCGGCAGCCTTAGATAGTGGGAAATAGGCTAGAGATGCTTTCAATGGCGGCCATTT 241  
 QY 220 AspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnPro 239  
 Db 242 GACATGCTCGATGGTCTTGTCCGATACAGTTCTTAACTTTCCAGTTGATATTCAGCCA 301  
 QY 240 PheArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPhe 259  
 Db 302 TTCAGAGATATGATGAGGAATGCGTATGGACTTGAGAAATCGAGATACAAAACCTTC 361  
 QY 260 AspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValPro 279  
 Db 362 GACGAACACTATACCTTATGTTATTATGTTGCTGTGTACGGTGGTGTGATGAGTGTCCA 421  
 QY 280 ValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeu 299  
 Db 422 ATTTGGGTATGCCCTCGAATCAAGGCAACCAACAGAGAGCGGTATATATGCTGTTTG 481  
 QY 300 AlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArg 319  
 Db 482 GCTCTGGGATGCCAATCAATTAACATACTACATACTCAGAGATGTTGGAGAAGTCCAGA 541  
 QY 320 ArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAsp 339  
 Db 542 AGAGGAAGATCTACTTGGCTCAAGATGAATTAGCACAGCGAGGTCTATCCGATGAAGAT 601  
 QY 340 IlePheAlaGlyArgValThrAspLysTyrArgAsnPhe 352  
 Db 602 ATATTTGCTGGAAGGTGACCGATAAATGGAGAATCTTT 640

RESULT 11  
 AW222027

LOCUS AW222027 676 bp mRNA linear EST 18-MAY-2001  
 DEFINITION EST2988938 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA

ACCESSION AW222027  
 VERSION AW222027.1 GI:6533711  
 KEYWORDS EST.

SOURCE tomato.

ORGANISM

Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE 1 (bases 1 to 676)

AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,  
 Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,  
 Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.  
 TITLE Generation of ESTs from tomato fruit tissue  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: CUGI

Clemson University Genomics Institute

Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.

FEATURES  
 Location/Qualifiers  
 source 1..676

/organism="Lycopersicon esculentum"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone\_lib="cLEN6L15"  
 /clone\_lib="tomato fruit red ripe, TAMU"  
 /tissue\_type="pericarp"

/dev\_stage="red ripe (7-20 days post-breaker)"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; supplier: Giovannoni; Fruit were tagged at the  
 breaker stage (first sign of lycopene accumulation on the  
 blossom end of the fruit) and harvested 7 days  
 post-breaker (fully red-ripe), 10 days post breaker, and  
 20 days post-breaker (over-ripe). 20 day fruit which  
 showed external or internal signs of pathogenesis were  
 discarded. Fruit were cut in half and the seeds and  
 locules were discarded prior to freezing the pericarp."

BASE COUNT 214 a 118 c 165 g 179 t  
 ORIGIN

Alignment Scores:

Pred. No.: 2.69e-118 Length: 676  
 Score: 1043.00 Matches: 201  
 Percent Similarity: 94.64% Conservative: 11  
 Best Local Similarity: 89.73% Mismatches: 12  
 Query Match: 45.95% Indels: 0  
 DB: 10 Gaps: 0

US-09-847-081B-2 (1-440) x AW222027 (1-676)

QY 189 LeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTrpGluThr 208  
 Db 2 CTGTGTGATGGCCCAACGCATCATATATACCCCGCAGCTTAGATAGTGGAAAT 61  
 QY 209 ArgLeuGluAspIlePheSerGlyArgPropheAspMetLeuAspAlaLeuSerAsp 228  
 Db 62 AGCTAGAGATGCTTTCAATGGCGGCCATTTGACATGCTCGATGCTGTGCTCGCAT 121  
 QY 229 ThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGlyMetArg 248  
 Db 122 ACAGTTTCTAACCTTCCAGTTGATATTCAGCCATTCAGAGATATGATGAGGAATCGGT 181  
 QY 249 MetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeuTyrLeuTyrCysTyr 268  
 Db 182 ATGGACTTGAGAAATCGAGATACAAAACCTTCGACGAACTATACCTTTATTGTTATTAT 241  
 QY 269 ValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGluSerLys 288  
 Db 242 GTTGTGCTGGTACGGTGGTGGTGTGAGTGTTCCAATTATGGGTATGCGCCCTGAATCAAG 301  
 QY 289 AlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThr 308  
 Db 302 GCAACACAGAGAGCGTATATATGCTGCTTGGCTCTGGGGATCGCAATCAATTAAC 361  
 QY 309 AsnIleLeuArgAspValGlyGluAspAlaArgGlyArgValTyrLeuProGlnAsp 328  
 Db 362 AACATCTCAGAGATGTTGGAGAAGATGCCAAGAGAGAGAGTCTACTTGCCTCAAGAT 421  
 QY 329 GluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGlyArgValThrAspLys 348  
 Db 422 GAATTAGCAGCAGCGGTCTATCCGATGAAGATATATTTCTGGAAGGGTGACCGATAA 481  
 QY 349 TrpArgAsnPheMetLysLysGlnIleGlnArgAlaArgLysPhePheAspGluSerGlu 368  
 Db 482 TGGAGATCTTTATGAGAAACAACATACATAGGCGCAAGAAAGTTCTTTGATGAGGAGAG 541  
 QY 369 LysGlyValThrGluLeuAspSerAlaSerArgTrpProValLeuThrAlaLeuLeu 388  
 Db 369 LysGlyValThrGluLeuAspSerAlaSerArgTrpProValLeuThrAlaLeuLeu 388



sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

BASE COUNT 200 a 105 c 160 g 169 t

ORIGIN

Alignment Scores:

Pred. No.: 1,21e-112 Length: 634  
Score: 997.00 Matches: 194  
Percent Similarity: 94.31% Conservative: 5  
Best Local Similarity: 91.94% Mismatches: 12  
Query Match: 43.92% Indels: 1  
DB: 13 Gaps: 0

US-09-847-081B-2 (1-440) x BM412533 (1-634)

QY 155 AlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArg 174  
DB 1 GCAGAGTATGCAAGACGCTTAACTAGGAACTATGCTAACTGCTCCGAGAGAAAGG 60  
QY 175 AlaLeuTyrAlaLeuTyrValTyrCysArgArgThrAspGluLeuValAspGlyProAsn 194  
DB 61 GCTATCTGGGCAATATATGATGGTGCAGAGAACAGATGAACCTTGTGTGATGGCCCAAC 120  
QY 195 AlaSerHisIleThrProGluAlaLeuAspArgTyrGluThrArgLeuGluAspIlePhe 214  
DB 121 GCATCATATATACCCGCGACCTTAGTAGTGGGAAATAGCTAGAGATGTTTC 180  
QY 215 SerGlyArgProPheAspMetLeuAspAlaLeuSerAspThrValSerArgPhePro 234  
DB 181 AATGGCGGCCATTTGACATGCTCGATGCTGCTTTGTCGATACAGTTCTTAACCTTCCA 240  
QY 235 ValAspIleGlnProPheArgAspMetIleGluGlyMetArgMetAspLeuTyrPheSer 254  
DB 241 GTTGATATTCAGCCATTACAGATATGATTGAAGAAATCGCTATGAGCTTGAGAAATCG 300  
QY 255 ArgTyrLysThrPheAspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGly 274  
DB 301 AGATACAAAACCTTCGAGCACTATACCTTATTGTTTATTGTTGCTGGTGGTGGG 360  
QY 275 LeuMetSerValProValMetGlyIleAlaProGluSerLysAlaThrThrGluSerVal 294  
DB 361 TTGATGAGTGTTCCTAATTATGGTATCGCCCTGAATCAAGGCAACACAGAGCGTA 420  
QY 295 TyrAsnAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspVal 314  
DB 421 TATATGCTGCTTTGGCTCTGGGGATCGCAATCAATTAACATACTACAGATGTT 480  
QY 315 GlyGluAspAlaArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGly 334  
DB 481 GGAGAGATGCCAGAGAGAGAGCTACTTGCCTCAAGATGAATAGCAGAGCAGGT 540  
QY 335 LeuSerAspGluAspIlePheAlaGlyArgValThrAspLysTyrPheAsnPheMetLys 354  
DB 541 CTATCCGATGAAGATATTTCTCGAAGGTGACCGATAATGAGAATCTTTATGAAG 600  
QY 355 LysGlnIleGlnArgAlaArgLysPheAsp 365  
DB 601 AAACAATA-CATAGGGGCGAAGATCTTTGAT 632

RESULT 14

BE460889

LOCUS

DEFINITION

ES\*412308 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA

clone CLG36H12, mRNA sequence.

ACCESSION

BE460889

VERSION

BE460889.1

KEYWORDS

EST.

SOURCE

tomato.

ORGANISM

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.  
1 (bases 1 to 600)  
Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Renning, C.M., Niernm, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.  
Generation of ESTs from tomato fruit tissue, breaker stage  
Unpublished (2000)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

TITLE  
JOURNAL  
COMMENT

FEATURES

source

1..600  
/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="CLG36H12"  
/clone\_lib="tomato breaker fruit, TIGR"  
/tissue\_type="pericarp"  
/dev\_stage="breaker"  
/lab\_host="SOLR"  
/note="Vector: pBluescriptSKmCuadapt; Site 1: EcoRI; Site 2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."  
BASE COUNT 178 a 99 c 157 g 166 t  
ORIGIN

Alignment Scores:

Pred. No.: 1.42e-110 Length: 600  
Score: 980.00 Matches: 185  
Percent Similarity: 95.98% Conservative: 6  
Best Local Similarity: 92.96% Mismatches: 8  
Query Match: 43.17% Indels: 0  
DB: 10 Gaps: 0

US-09-847-081B-2 (1-440) x BE460889 (1-600)

QY 137 ProGlyAsnLeuGlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGlu 156  
DB 3 CGGGGAATTTGGGCTTGTGTGAGTGAATCATATGATGAGTGTGCTGAAGTGTGTGCAGAG 62  
QY 157 TyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIle 176  
DB 63 TATGCAAGACGCTTAACTTAGGAACATATGCTAACTCCCGAGAGAGAGGGCTATC 122  
QY 177 TrpAlaIleTyrValTyrCysArgArgThrAspGluLeuValAspGlyProAsnAlaSer 196  
DB 123 TGGGCAATATATGATGTCGAGAGAACAGATGAACCTTGTGATGCCCAACGATCA 182  
QY 197 HisIleThrProGlnAlaLeuAspArgTyrGluThrArgLeuGluAspIlePheSerGly 216  
DB 183 TATATTACCCCGGACGCTTAGTAGTGGGAAATAGGCTAGAAATGTTTCAATGGG 242  
QY 217 ArgProPheAspMetLeuAspAlaLeuSerAspThrValSerArgPheProValAsp 236  
DB 243 CGGCCATTGACATGCTCGATGCTGCTTGTGCTGATACAGTTCTTAACCTTCCAGTTGAT 302  
QY 237 IleGlnProPheArgAspMetIleGluGlyMetArgMetAspLeuTyrPheSerArgTyr 256  
DB 303 ATTCAGCCATTCAGAGATATGATTGAAGGAATCGGACTTGAGAAATCGAGATAC 362  
QY 257 LysThrPheAspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMet 276  
DB 363 AAAAATTCGACGAACTATACCTTTATTGTTTATGTTGCTGCTGAGTGGTGGTGGTGGT 422  
QY 277 SerValProValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsn 296

```

|||||...|||||
Db 423 AGTGTTCCTAATATGGGTATGCCCTGAATCAAGGCAACACAGAGCGCTATATAT 482
QY 297 AlalaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleuArgAspValGlyGlu 316
Db 483 GTGTCTTTGGCTCTGGGGTCCCAATCAATTAACATACTACAGAGATGTTGGAGAA 542
QY 317 AspAlaArgArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeu 335
Db 543 GATGCCAGAGAGGAGAGAGTCTACTTGGCTCAAGATGAATTAGCAGACGAGTCTA 599

RESULT 15
BE432511
LOCUS
DEFINITION
  ESR399040 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
  clone cLE8H5, mRNA sequence.
ACCESSION
  BE432511
VERSION
  BE432511.1 GI:9430354
KEYWORDS
  EST.
SOURCE
  tomato.
ORGANISM
  Lycopersicon esculentum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
  Lycopersicon.
REFERENCE
  1 (bases 1 to 623)
  Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
  Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Renning,C.M.,
  Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
  ,S.D.
  Generation of ESTs from tomato fruit tissue, breaker stage
  Unpublished (2000)
  Contact: CUGI
  Clemson University Genomics Institute
  Clemson University
  100 Jordan Hall, Clemson, SC 29634, USA
  Email: http://www.genome.clemson.edu/orders/index.html
  5 prime sequence.
FEATURES
  source
    location/Qualifiers
      1..623
        /organism="Lycopersicon esculentum"
        /cultivar="TA496"
        /db_xref="taxon:4081"
        /clone="cLE8H5"
        /clone_lib="tomato breaker fruit, TIGR"
        /tissue_type="Pericarp"
        /dev_stage="breaker"
        /lab_host="SOLR"
        /note="Vector: pBluescriptSMCvadap; Site_1: EcorI;
        Site_2: XhoI; Fruit were harvested at the breaker stage
        (first sign of lycopen accumulation on the blossom end of
        the fruit). Fruit were cut in half and the seeds and
        locules were discarded prior to freezing the pericarp."
BASE COUNT
  191 a 101 c 164 g 167 t
ORIGIN

```

## Alignment Scores:

```

Pred. No.:      3,08e-110      Length:      623
Score:          977.50         Matches:    190
Percent Similarity: 94.20%      Conservative: 5
Best Local Similarity: 91.79%   Mismatches: 10
Query Match:    43.06%         Indels:     2
DB:             10            Gaps:       1

```

US-09-847-081B-2 (1-440) x BE432511 (1-623)

```

QY 145 GluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyrLeuGly 164
|||||...|||||
Db 3 GAAGCATATGATAGGTGTGGTGAAGTATGTGCAGAGATATGCAGAGACGTTTAACATTAGGA 62
QY 165 ThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIleTyrValTyrCysArg 184
|||||...|||||
Db 63 ACTATGCTAATGACTCCCGAGAGAGAGGGCTATCTGGGCAATATATGTTGTCGACA 122

```

```

QY 185 ArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAsp 204
Db 123 AGACAGATGAACACTTGTGTGATGGCCCAACGATCATATATTACCCCGCAGCCTTAGAT 182
QY 205 ArgTTPGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAla 224
Db 183 AGTGGGAAATAGGCTAGAGATGTTTCAATGGGGGCCCATTTGCACATGCTCGATGGT 242
QY 225 AlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIle 244
Db 243 GCTTTGTCCGATACAGTTTCTTAACTTCCAGTTGATATTACGCCATTTCAGAGATATGATT 302
QY 245 GluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeuTyrLeu 264
Db 303 GAAGGAATCGGTATGGACTTTGAGAAATCGAGATACAAAAACTTCGACGAACTATACCTT 362
QY 265 Tyr---Cys-TyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIle 283
Db 363 TATTGGTTAAATTTATGTGCTGGTACGGTTGGGTTCATGAGTGTTCCTCAATTATGGGTAT 422
QY 283 ealaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLe 303
Db 423 CGCCCTGAATCAAAGGCAACAAACAGAGAGCGTATATATGCTGCTTGGCTCTGGGAT 482
QY 303 uAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgGlyArgVa 323
Db 483 CGCAATCAATTAACATAACATCTCAGAGATGTTGGAGAAGATGCCAGAGAGAGAGAT 542
QY 323 lTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaG1 343
Db 543 CTACTTGGCTCAAGATGAATTAGCAGACGAGGTCTATCCGATGAAGATATATTGCTGG 602
QY 343 yArgValThrAspLysTrp 349
Db 603 GAGGGTGACCGATAAATGG 621

```

Search completed: April 5, 2003, 04:26:44  
Job time : 1532 secs